Genetic diversity in the Dutch harness horse population using pedigree analysis

A. Schurink [a,*], D.J.G. Arts [b], B.J. Ducro [a]

[a] Animal Breeding and Genomics Centre, Wageningen University, P.O. Box 338, 6700 AH Wageningen, The Netherlands
[b] Royal Dutch Warmblood Studbook (KWPN), P.O. Box 156, 3840 AD Harderwijk, The Netherlands

ABSTRACT

The Royal Dutch Warmblood Studbook consists of several types with different population sizes. The harness horse population, one of the types, is for several reasons suspected of substantial inbreeding. Since 2005 the studbook started applying measures to reduce inbreeding in the harness horse population. The aim of our study was to investigate the genetic diversity in the Dutch harness horse population. Furthermore, we determined whether attempts to reduce inbreeding in the Dutch harness horse population were successful. Pedigree of harness horses contained 54,170 individuals and 3568 founders. Various parameters (e.g. inbreeding coefficient and rate, effective number of founders, ancestors and founder genomes) were calculated and birth year cohorts from 1950 to 2009 were made to assess genetic diversity in the harness horse population over time. Number of foals registered annually was on average 1310 since 1980. Average generation interval was 8.6 years, average inbreeding coefficient of cohort 2005–2009 was 0.080 (SD = 0.042) and mean inbreeding rate was 0.0136. A distinct loss of genetic diversity was found during the seventies. A clear bottleneck was observed from cohort 1965–1969 to cohort 1970–1974 probably related to selection of specific families and the establishment of the Royal Dutch Warmblood Studbook in 1970 after merging many regional studbooks. In cohort 2005–2009 only 4 ancestors accounted for 50% of the current gene pool of the Dutch harness horse population. The major loss of genetic diversity (4.6%) was caused by bottlenecks. Introgression of the Hackney horse breed within the Dutch harness horse population was substantial and steadily increased from 4.2% in 1980 to 21.1% in 2009. Introgression of the American Saddlebred breed was at a maximum of 4.5%, but diminished to <1% in recent years. Hackney horse stallions had limited relatedness to harness horse broodmares and stallions, though broodmares and harness horse stallions were reasonably related. Inbreeding (coefficient) rate within the Dutch harness horse population exceeded the 0.01 per generation FAO limit, though efforts made by the studbook to reduce inbreeding seem successful, as average inbreeding coefficient stabilized during recent years and even dropped substantially in 2009. However, the studbook should continuously pay attention in order to prevent further losses of genetic diversity. Various efforts could reduce inbreeding in the population like introduction of stallions from other breeds (e.g. unrelated Hackney horses), deliberate mate selection and limit breeding of particular sires.

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1. Introduction

The Royal Dutch Warmblood Studbook (KWPN) is an open studbook. Horses from other breeds can therefore enter the studbook provided that these horses fit the breeding goal, which is assessed during inspections. The KWPN population consists of several types: riding horses, harness horses (~10% of the horses) and Gelder horses (~4% of the horses). Breeding is often within the harness horse type; 83.5% of harness horses descend from a harness horse sire and harness horse dam. Also, 95.2% of offspring from a harness horse sire

* Corresponding author. Tel.: +31 317 482207; fax: +31 317 483929.
E-mail address: Anouk3.Schurink@wur.nl (A. Schurink).

is registered as harness horse and 84.7% of offspring from a harness horse dam is registered as a harness horse. Breeding within type most likely led to population subdivision, which might have increased inbreeding within subpopulations (e.g. Falconer and Mackay, 1996). Unequal contribution of founders and ancestors might decrease genetic diversity as well (Boichard et al., 1997; Lacy, 1989). Certain ancestors are marked by the studbook as influential based on their contribution to the population (KWPN, 2004). A particular sire born in 1950 covered 1273 mares, sired 13 approved sons, and is considered to be the founding stallion of the current Dutch harness horse population (KWPN, 2004). Another influential ancestor born in 1975 sired 15 approved sons (KWPN, 2004) of which some are still used in breeding. Also, the current active harness horse breeding population consists of roughly 30 approved harness horse stallions and 1100 broodmares. Harness horses are selected on performance in driving, health, conformation and temperament and are known for their spectacular movement. Small population size and selection are known to reduce genetic diversity (e.g. Falconer and Mackay, 1996). The harness horse population is therefore suspected of substantial inbreeding, although in the course of time Hackney horse stallions and American Saddlebred stallions were introduced to increase genetic diversity.

Inbreeding generally reduces performance, health and fertility of an individual (e.g. Falconer and Mackay, 1996; Sairanen et al., 2009; Sevinga et al., 2004; Van Eldik et al., 2006) and should therefore be restricted. To prevent negative effects of inbreeding, FAO (1998) set a maximum inbreeding (coefficient) rate of 0.01 per generation. Analysis of inbreeding in the harness horse population in 2004 indicated that the inbreeding rate exceeded 0.01. Since 2005 the studbook started applying measures to reduce inbreeding in the harness horse population. Measures to reduce inbreeding concern informing and involving breeders by means of a more active and intensive use of breeding advices. Also, harness horse breeders annually receive a letter which states the kinship of their broodmare(s) to all approved harness horse stallions. Moreover, during inspection positive discrimination is applied to stallions unrelated or with limited relationship to the current harness horse population. The aim of our study was to investigate the genetic diversity in the Dutch harness horse population. Furthermore, we determined whether attempts to reduce inbreeding in the Dutch harness horse population applied by the KWPN studbook since 2005 were successful.

2. Materials and methods

2.1. Pedigree

The complete KWPN pedigree file included 458,352 horses belonging to the various types. Pedigree of harness horses (n = 42,005 individuals registered as harness horse) contained 54,170 individuals (from several types); 31,337 females (57.8%) and 22,833 males (42.2%). In total 3568 horses had unknown parents and were therefore by definition considered to be founders. Founders were registered as riding horse (75.7%), Gelder horse (6.6%), harness horse (3.5%) and unknown (14.2%). The remaining 50,602 horses descended from 3255

sires and 18,584 dams; 43 horses had an unknown sire only and 326 horses had an unknown dam only. Number of offspring per sire ranged from 1 to 1334. In total 56.5% of sires had 1 offspring and 7.1% had 25 or more offspring. Number of offspring per dam ranged from 1 to 20. In total 52.2% of dams had 1 offspring and 13.2% had 5 or more offspring.

Missing birth dates of horses (n = 9915) were arbitrarily set to 9 years before the average birth year of its offspring. Birth year varied from 1854 to 2009, though only 4 horses were born before 1900. Generation interval was calculated as the average age of the parents when their reproducing offspring are born (Boichard, 2002; Falconer and Mackay, 1996). Percentage of known ancestors per ancestral generation (Boichard, 2002) and number of equivalent complete generations traced ($= \sum (1/2)^n$ over all generations, where n is the number of generations separating horses from each known ancestor; Maignel et al., 1996) were used to judge the pedigree quality and depth.

2.2. Genetic diversity parameters

Birth year cohorts were made (Table 1) to assess genetic diversity in the harness horse population over time. The studbook applied measures to reduce inbreeding since 2005. Therefore the most recent birth year cohort was 2005–2009 and was considered to be the reference population. To allow comparison with cohort 2005–2009 other birth year cohorts comprised 5 years as well.

Various parameters were calculated to assess genetic diversity in the harness horse population: inbreeding coefficient, rate of inbreeding, effective number of founders, effective number of ancestors, ratio of effective number of founders over effective number of ancestors, effective number of founder genomes, ratio of effective number of founders over effective number of founder genomes, influential founders, influential ancestors and average relatedness within and between various groups of the harness horse population.

2.2.1. Inbreeding

Inbreeding is the mating of related individuals. Inbreeding coefficient of an individual is defined as the probability that

Table 1
Genetic diversity parameters per birth year cohort. Number of registered harness horses (N), average inbreeding coefficient ($\bar{F}_i$), effective number of founders (f_e), effective number of ancestors (f_a), effective number of founder genomes (N_g), ratio of effective number of founders over effective number of ancestors (f_e/f_a) and ratio of effective number of founders over effective number of founder genomes (f_e/N_g) per birth year cohort.

Cohort	N	$\bar{F}_i$	f_e	f_a	N_g	f_e/f_a	f_e/N_g
1950–1954	1221	0.006	406.2	123.9	70.7	3.3	5.7
1955–1959	1537	0.008	395.9	108.5	63.6	3.6	6.2
1960–1964	1400	0.014	316.4	74.3	46.1	4.3	6.9
1965–1969	1677	0.017	321.9	66.8	42.0	4.8	7.7
1970–1974	1770	0.025	158.6	22.3	16.1	7.1	9.9
1975–1979	2557	0.037	109.1	14.4	10.5	7.6	10.4
1980–1984	7067	0.051	92.6	11.8	8.6	7.8	10.8
1985–1989	6250	0.062	85.8	10.7	7.7	8.0	11.1
1990–1994	8209	0.065	87.6	10.8	7.2	8.1	12.2
1995–1999	6485	0.074	90.7	10.3	6.3	8.8	14.4
2000–2004	6061	0.082	92.6	9.5	5.8	9.7	16.0
2005–2009	5227	0.080	98.6	9.8	5.5	10.1	17.9